BIOTECHNOLOGY SYSTEMS BRANCH

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Application Serial Number: _10/083,720_

Source: _OIPE_

Date Processed by STIC: _3/27/02_

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Revised 01/29/2002

OIPE

RAW SEQUENCE LISTING   DATE: 03/27/2002
PATENT APPLICATION: US/10/083,720   TIME: 14:15:08

Input Set : A:\DX0644KBK 28FEB2002.ST25.txt
Output Set: N:\CRF3\03272002\J083720.raw

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   3 <110> APPLICANT: de Waal Malefyt, Rene
   4        Fickenscher, Helmut
   5        Fleckenstein, Bernhard
   6        Knappe, Andrea
   8 <120> TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
  10 <130> FILE REFERENCE: DX0644KBK
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/083,720
C--> 12 <141> CURRENT FILING DATE: 2002-02-28
  12 <150> PRIOR APPLICATION NUMBER: 09/363,993
  13 <151> PRIOR FILING DATE: 1999-07-29
  15 <160> NUMBER OF SEQ ID NOS: 21
  17 <170> SOFTWARE: PatentIn version 3.1
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 1076
  21 <212> TYPE: DNA
  22 <213> ORGANISM: Homo sapiens
  24 <220> FEATURE:
  25 <221> NAME/KEY: CDS
  26 <222> LOCATION: (36)..(548)
  27 <223> OTHER INFORMATION:
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  32                                         Met Leu Val Asn Phe Ile
  33                                         1               5
  35 ttg agg tgt ggg ttg ctg tta gtc act ctg tct ctt gcc att gcc aag    101
  36 Leu Arg Cys Gly Leu Leu Leu Val Thr Leu Ser Leu Ala Ile Ala Lys
  37             10              15                  20
  39 cac aag caa tct tcc ttc acc aaa agt tgt tac cca agg gga aca ttg    149
  40 His Lys Gln Ser Ser Phe Thr Lys Ser Cys Tyr Pro Arg Gly Thr Leu
  41         25                  30                  35
  43 tcc caa gct gtt gac gct ctc tat atc aaa gca gca tgg ctc aaa gca    197
  44 Ser Gln Ala Val Asp Ala Leu Tyr Ile Lys Ala Ala Trp Leu Lys Ala
  45      40                  45                  50
  47 acg att cca gaa gac cgc ata aaa aat ata cga tta tta aaa aag aaa    245
  48 Thr Ile Pro Glu Asp Arg Ile Lys Asn Ile Arg Leu Leu Lys Lys Lys




  55 tcc ttc ttc atg gaa gac gtt ttt ggt caa ctg caa ttg caa ggc tgc    441
  56 Ser Phe Phe Met Glu Asp Val Phe Gly Gln Leu Gln Leu Gln Gly Cys
  57             90                  95                  100
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Input Set : A:\DX0644KBK 28FEB2002.ST25.txt
Output Set: N:\CRF3\03272002\J083720.raw

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60 Lys Lys Ile Arg Phe Val Glu Asp Phe His Ser Leu Arg Gln Lys Leu
61         105               110                115
63 agc cac tgt att tcc tgt gct tca tca gct aga gag atg aaa tcc att      437
64 Ser His Cys Ile Ser Cys Ala Ser Ser Ala Arg Glu Met Lys Ser Ile
65         120               125               130
67 acc agg atg aaa aga ata ttt tat agg att gga aac aaa gga atc tac      485
68 Thr Arg Met Lys Arg Ile Phe Tyr Arg Ile Gly Asn Lys Gly Ile Tyr
69 135               140               145               150
71 aaa gcc atc agt gaa ctg gat att ctt ctt tcc tgg att aaa aaa tta      533
72 Lys Ala Ile Ser Glu Leu Asp Ile Leu Leu Ser Trp Ile Lys Lys Leu
73             155               160               165
75 ttg gaa agc agt cag taaaccaaag ccaagtacat tgattttaca gttattttga     588
76 Leu Glu Ser Ser Gln
77             170
79 aatacaataa gaactgctag aaatatgttt ataacagtct atttctttta aaaacttttt    648
81 aacataatac tgacggcatg ttaggtgatt cagaatagac aagaaggatt tagtaaatta    708
83 acgttttgga tataagttgt cactaatttg cacattttct gtgttttcaa ataatgtttc    768
85 cattctgaac atgttttgtc attcacaagt acattgtgtc aacttaattt aaagtatgta    828
87 acctgaatta actcgtgtaa tatttgtgtg tggagtggga tgtgggggt ggaggggaa      888
89 tgacagattt ctggaatgca atgtaatgtt actgagactt aaatagatgt tatgtatatg    948
91 attgtctgtt taagtgtttg aaaattgtta attatgccca gtgtgaactt agtacttaac   1008
93 acattttgat tttaattaaa taaattgggt ttccttctca aaaaaaaaaa aaaaaaaaaa   1068
95 aaaaaaaa                                                            1076
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99 <211> LENGTH: 171
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 2
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106 1               5               10               15
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110             20               25               30
113 Tyr Pro Arg Gly Thr Leu Ser Gln Ala Val Asp Ala Leu Tyr Ile Lys
114         35               40               45
117 Ala Ala Trp Leu Lys Ala Thr Ile Pro Glu Asp Arg Ile Lys Asn Ile
118     50               55               60
121 Arg Leu Leu Lys Lys Lys Thr Lys Lys Gln Phe Met Lys Asn Cys Gln
122 65               70               75               80
125 Phe Gln Glu Gln Leu Leu Ser Phe Phe Met Glu Asp Val Phe Gly Gln
126             85               90               95
129 Leu Gln Leu Gln Gly Cys Lys Lys Ile Arg Phe Val Glu Asp Phe His
130             100               105               110
133 Ser Leu Arg Gln Lys Leu Ser His Cys Ile Ser Cys Ala Ser Ser Ala
134         115               120               125
137 Arg Glu Met Lys Ser Ile Thr Arg Met Lys Arg Ile Phe Tyr Arg Ile
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149 <210> SEQ ID NO: 3
150 <211> LENGTH: 179
151 <212> TYPE: PRT
152 <213> ORGANISM: Equine Herpes Virus
154 <400> SEQUENCE: 3
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157 1               5                  10                  15
160 Trp Ala Asp Asn Lys Tyr Asp Ser Glu Ser Gly Asp Asp Cys Pro Thr
161             20                  25                  30
164 Leu Pro Thr Ser Leu Pro His Met Leu His Glu Leu Arg Ala Ala Phe
165         35                  40                  45
168 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Met
169     50                  55                  60
172 Leu Leu Asp Gly Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
173 65                  70                  75                  80
176 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
177             85                  90                  95
180 Gln Ala Glu Asn His Ser Thr Asp Gln Glu Lys Asp Lys Val Asn Ser
181             100                 105                 110
184 Leu Gly Glu Lys Leu Lys Thr Leu Arg Val Arg Leu Arg Arg Cys His
185         115                 120                 125
188 Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys
189     130                 135                 140
192 Ser Ala Phe Ser Lys Leu Gln Glu Lys Gly Val Tyr Lys Ala Met Ser
193 145                 150                 155                 160
196 Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Thr Lys
197             165                 170                 175
200 Met Lys Asn
204 <210> SEQ ID NO: 4
205 <211> LENGTH: 170
206 <212> TYPE: PRT
207 <213> ORGANISM: Epstein Barr Virus
209 <400> SEQUENCE: 4
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216             20                  25                  30
219 Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
220         35                  40                  45
223 Gln Thr Lys Asp Glu Val Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
224     50                  55                  60
227 Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile
228 65                  70                  75                  80
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240          115                    120                    125
243 Ser Lys Ala Val Glu Gln Ile Lys Asn Ala Phe Asn Lys Leu Gln Glu
244      130                    135                    140
247 Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
248 145                    150                    155                    160
251 Ile Glu Ala Tyr Met Thr Ile Lys Ala Arg
252                    165                    170
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 178
257 <212> TYPE: PRT
258 <213> ORGANISM: Mus musculus
260 <400> SEQUENCE: 5
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263 1                    5                    10                    15
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267                    20                    25                    30
270 Phe Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe
271          35                    40                    45
274 Ser Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile
275      50                    55                    60
278 Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys
279 65                    70                    75                    80
282 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro
283                    85                    90                    95
286 Gln Ala Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu
287                    100                    105                    110
290 Gly Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg
291          115                    120                    125
294 Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser
295      130                    135                    140
298 Asp Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu
299 145                    150                    155                    160
302 Phe Asp Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met
303                    165                    170                    175
306 Lys Ser
310 <210> SEQ ID NO: 6
311 <211> LENGTH: 178
312 <212> TYPE: PRT
313 <213> ORGANISM: Homo sapiens
315 <400> SEQUENCE: 6
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318 1                    5                    10                    15
321 Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
322          20                    25                    30
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RAW SEQUENCE LISTING   DATE: 03/27/2002
PATENT APPLICATION: US/10/083,720   TIME: 14:15:08

Input Set : A:\DX0644KBK 28FEB2002.ST25.txt
Output Set: N:\CRF3\03272002\J083720.raw

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334 65                    70                  75                  80
337 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
338                    85                  90                  95
341 Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
342                    100                 105                 110
345 Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
346         115                 120                 125
349 Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
350         130                 135                 140
353 Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
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361 Arg Asn
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367 <212> TYPE: DNA
368 <213> ORGANISM: synthetic
370 <400> SEQUENCE: 7
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375 <211> LENGTH: 26
376 <212> TYPE: DNA
377 <213> ORGANISM: Synthetic
379 <400> SEQUENCE: 8
380 tgcactgaca tctaagttct ttagca                                     26
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384 <211> LENGTH: 28
385 <212> TYPE: DNA
386 <213> ORGANISM: Synthetic
388 <400> SEQUENCE: 9
389 tggcaaaact gcaccttcac acagagct                                   28
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394 <212> TYPE: DNA
395 <213> ORGANISM: Synthetic
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404 <213> ORGANISM: Synthetic
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415 <400> SEQUENCE: 12
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VERIFICATION SUMMARY   DATE: 03/27/2002
PATENT APPLICATION: US/10/083,720   TIME: 14:15:09

Input Set : **A:\DX0644KBK 28FEB2002.ST25.txt**
Output Set: **N:\CRF3\03272002\J083720.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10 /083,720

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
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9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.